REMARKS/ARGUMENTS

Status of the Application

In the July 28, 2006, Non-Final Office Action, claims 27-29 and 32-38 were rejected, claims 30-31 were objected to, and claim 39 was withdrawn from consideration. In the present response, withdrawn claim 39 was amended to put this claim in condition for rejoinder if the product claim 35 is allowed.

Thus, claims 27-38 are pending. No new matter was added.

Applicants thank the Examiner for the notation that claims 30-31 would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claim.

Specification

The previously amended paragraph at page 1, lines 4-7, has been currently amended to indicate the status of the prior applications.

Two paragraphs have been amended to correct the given size of the amino acid sequence of the rice DRAP1 protein (SEQ ID NO:32) encoded by rls12.pk0015.e12. In the paragraph beginning at page 6, line 33, and continuing through page 7, line 16, and the paragraph beginning at page 33, line 21, and continuing through page 34, line 7, reference is made to the size of the rice DRAP1 protein (SEQ ID NO:32) as being 259 amino acids. However, as shown in the Sequence Listing, SEQ ID NO:32 actually contains 258 amino acids. This error by Applicants was due to inclusion of the stop codon as encoding the terminal "amino acid". The coding region of 777 bp for clone rls12.pk0015.e12, cited on page 33, line 22, corresponds to a translation of bases 55-831 of SEQ ID NO:31, wherein bases 829-831 encode the stop codon (codon number 259). Correction of this error does not affect the content of the originally-submitted sequence listing or the claims.

The paragraph beginning at page 40, line 30, and continuing through page 41, line 11, has been amended to correct the size of the carboxy-terminal deletion of DRAP1 sequence in the clone, p35S::Gal4/rDRAP1Y75. The size of the deletion was stated in the original application to be 166 amino acids; however, the actual size of the deletion was really 184 amino acids. This mathematical error by Applicants occurred while drafting the application. In support, Applicants point to page 41, lines 4-11, and note the designation "Y75" in the clone name designating the first amino

acid, a tyrosine, of DRAP1 that is deleted. Similarly, Applicants note that the two other clones mentioned in the same paragraph, with *correct* amino acid deletion sizes of 111 and 136 amino acids, relate to deletions beginning at amino acid R148, an arginine, and S123, a serine, respectively. Deletion of amino acids 75-258 corresponds to a deletion of 184 amino acids, not 166 amino acids. Correction of this error in the text of the specification serves to make the specification consistent with the original submitted sequence listing, and thus Applicants assert that no new matter is added by this correction.

The paragraph at page 41, lines 12-20, has been amended to correct errors related to the size of the deletion of DRAP1 in the clone, p35S::Gal4/rDRAP1Y75, and to the total size of rice DRAP1 (SEQ ID NO:32), that is, 258 amino acids instead of 259 amino acids. First, the reference to the 166 amino acid deletion is replaced by reference to the 184 amino acid deletion, as explained above. Second, the reference to 123 amino acids in an N-terminal rice DRAP1 fragment is replaced, in two places, by reference to the 122 amino acid N-terminal fragment; this number corresponding to the subtraction of the 136 amino acid deletion of clone p35S::Gal4/rDRAP1S123 from the total size, 258 amino acids, of the rice DRAP1 (SEQ ID NO:32). Third, the reference to the region "between 93 and 123" is replaced by reference to the region "between 74 and 123", wherein the N-terminal region of 74 amino acids corresponds to beginning of the deletion at amino acid position 75 in the clone, p35S::Gal4/rDRAP1Y75 (the "75" in the clone name indicates the beginning of the deletion). Finally, the size of the region "between 74 and 123" is corrected to "48 amino acids".

Applicants believe no new matter has been added through correction of these clerical errors.

Rejections Under 35 U.S.C. § 112, 1st Paragraph

Claims 27-29 and 32-38 were rejected under 35 U.S.C. § 112, 1st Paragraph, as failing to comply with the written description requirement for containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Applicants respectfully traverse these rejections.

Applicants describe a rice DRAP1 protein having the amino acid sequence of SEQ ID NO:32. This rice DRAP1 protein has transcriptional repressor activity and binds to the rice DR1 protein (SEQ ID NO:10). Additionally, by use of deletion studies (Example 6), Applicants have shown that the amino-terminal 122 amino acids of DRAP1 retains transcriptional repressor activity (page 40, second paragraph) and that amino acids 13-93 are required for DR1-binding activity (page 37, first paragraph).

Applicants also have described DRAP1 proteins from corn (SEQ ID NO:28), soybean (SEQ ID NO:34) and wheat (SEQ ID NO:40). There is very high sequence homology among the monocot DRAP1 proteins. Appendices A1-A2[1] show a sequence alignment of the following: the full-length DRAP1 proteins from corn, rice and wheat; and the N-terminal regions of the corn, rice and wheat DRAP1 proteins. The amino acid sequence of the N-terminal region of these three monocot DRAP1 proteins is highly conserved, as shown in Appendix B. The 122-aa N-terminal region of the rice DRAP1 protein is 92.5% and 88.3% identical with the corresponding N-terminal regions of the corn and wheat DRAP1 proteins, respectively.

The specification (page 33) notes that the N-terminal region of the rice DRAP1 protein has a histone fold-like structure located from residue 9 to 84. The Office Action cites Baxevanis et al., 1998, as disclosing that proteins having histone-fold motifs do not have readily identifiable primary structures. Applicants submit that the description of amino acid sequences of four plant DRAP1 proteins provides guidance as to which amino acid residues can be varied in the critical N-terminal region of the protein.

Applicants submit that the above information indicates that Applicants were in possession of the invention as currently claimed. Consequently, Applicants respectfully request withdrawal of the 35 U.S.C. § 112, first paragraph, written description rejection.

Claims 27-29 and 32-38 were rejected under 35 U.S.C. § 112, 1st Paragraph, because the specification, while being enabling for an isolated polynucleotide encoding the amino acid sequence of SEQ ID NO:32, a chimeric gene and a vector

[1] The amino acid sequence alignment was obtained using the Clustal method of alignment with the default parameters, as described in the specification. Amino acid residues that differ from SEQ ID NO:32 are enclosed in boxes. A consensus sequence, "Consensus #1", shows the residue of SEQ ID NO:32 when all amino acids at that position match the residue of SEQ ID NO:32.

comprising said isolated polynucleotide, a method for transforming a cell comprising introducing said isolated polynucleotide and a plant and seed comprising said chimeric genes, does not reasonably provide enablement for an isolated polynucleotide comprising a nucleotide sequence encoding a polypeptide having transcriptional repressor activity, wherein the amino acid sequence of said polypeptide and the amino acid sequence of SEQ ID NO:32 have at least 85-95% identity based on the Clustal alignment method. Applicants respectfully traverse these rejections.

As noted above, Applicants have determined through deletion studies that the 122-aa N-terminal region of SEQ ID NO:32 retains transcriptional repressor activity. Applicants have also disclosed corn (SEQ ID NO:28) and wheat (SEQ ID NO:40) amino acid sequences that have N-terminal regions with 92.5% and 88.3% sequence identity, respectively, with the corresponding 122-aa N-terminal region of SEQ ID NO:32. Applicants submit that these plant amino acid sequences provide guidance for one skilled in the art to make and practice the claimed invention.

The Office Action notes that the structure of the rice DRAP1 protein is intimately associated functionally with the structure of the rice DR1 protein to regulate function of RNA polymerase II in a rice cell. In several characterized non-plant systems, the DRAP1 protein acts as a co-repressor, that is, it does not have repressor activity on its own. Applicants note that the rice DRAP1 protein functions independently as a repressor, although its repressor activity can be enhanced by association with rice DR1 protein. This association, however, is not required for the invention as claimed, which is directed to a polypeptide having transcriptional repressor activity.

In light of the above remarks, Applicants submit that the specification would enable a person skilled in the art to practice the invention as currently claimed. Consequently, Applicants respectfully request withdrawal of the 35 U.S.C. § 112, first paragraph, enablement rejection.

Summary

In view of the foregoing amendments and remarks, Applicants submit that this application is in condition for allowance. In order to expedite disposition of this case, the Examiner is invited to contact Applicants' representative at the telephone number

below to resolve any remaining issues. Should there be a fee due which is not accounted for, please charge such fee to Deposit Account No. 501447 (Potter Anderson & Corroon LLP).

Respectfully submitted,

By: _____

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